

OM protein - protein search, using sw model

Run on: April 15, 2005, 15:29:10 ; Search time 175 Seconds
 (without alignments)
 327.089 Million cell updates/sec

Title: US-09-825-423C-3
 Perfect score: 766
 Sequence: 1 GSHMSPVFTDNSSPPAVPQS.....TVLDQAETAGARLVVLATAT 148

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	743	97.0	263	5	ABB77261	Abb77261 HCV bait
2	743	97.0	631	2	AAW93482	Aaw93482 HCV NS3 p
3	743	97.0	638	4	AAE10068	Aae10068 Hepatitis
4	743	97.0	685	2	AAW71271	Aaw71271 Protein e
5	743	97.0	687	2	AAR79223	Aar79223 pHCV150-e
6	743	97.0	1648	2	AAR79221	Aar79221 pHCV176-e
7	743	97.0	1986	8	ADR38451	Adr38451 Hepatitis
8	743	97.0	2202	6	AAO26783	Aao26783 Protein d
9	743	97.0	2631	6	AAO26785	Aao26785 Protein d

10	743	97.0	2984	4	AAE00447	Aae00447	Hepatitis
11	743	97.0	2984	4	AAE00442	Aae00442	Hepatitis
12	743	97.0	3002	7	ADM24822	Adm24822	Hepatitis
13	743	97.0	3011	2	AAR40119	Aar40119	HCV genom
14	743	97.0	3011	2	AAR79232	Aar79232	HCV seque
15	743	97.0	3011	2	AAW77397	Aaw77397	Hepatitis
16	743	97.0	3011	2	AAW77398	Aaw77398	Hepatitis
17	743	97.0	3011	2	AAW98021	Aaw98021	Infectiou
18	743	97.0	3011	2	AAW98020	Aaw98020	Infectiou
19	743	97.0	3011	4	AAB31169	Aab31169	Amino aci
20	743	97.0	3011	5	AAU99290	Aau99290	Hepatitis
21	743	97.0	3011	5	AAU79221	Aau79221	Hepatitis
22	743	97.0	3011	6	AAO26784	Aao26784	Protein d
23	743	97.0	3011	6	ABP71460	Abp71460	Amino aci
24	743	97.0	3011	6	ABU61849	Abu61849	HCV-H. 8/
25	743	97.0	3011	8	ADH79949	Adh79949	E2 HCV en
26	743	97.0	3011	8	ADJ56744	Adj56744	Hepatitis
27	743	97.0	3011	8	ADJ64256	Adj64256	Hepatitis
28	743	97.0	3011	8	ADL72983	Adl72983	Hepatitis
29	743	97.0	3012	5	AAU99289	Aau99289	Hepatitis
30	743	97.0	3012	6	ABU61848	Abu61848	HCV H77 c
31	743	97.0	3015	4	AAB30733	Aab30733	Amino aci
32	743	97.0	3015	4	AAB30731	Aab30731	Amino aci
33	743	97.0	3015	4	AAB30730	Aab30730	Amino aci
34	743	97.0	3015	4	AAB30732	Aab30732	Amino aci
35	743	97.0	3180	6	ABG73195	Abg73195	MKO-Z vir
36	743	97.0	3208	7	ADD67948	Add67948	Hepatitis
37	742	96.9	279	3	AAy43881	Aay43881	Amino aci
38	742	96.9	318	3	AAy43895	Aay43895	Amino aci
39	742	96.9	3011	2	AAR40120	Aar40120	HCV genom
40	742	96.9	3011	5	AAU84597	Aau84597	HCV polyp
41	741	96.7	3011	2	AAR66995	Aar66995	Hepatitis
42	739	96.5	279	3	AAy43891	Aay43891	Amino aci
43	739	96.5	279	3	AAy43889	Aay43889	Amino aci
44	738	96.3	246	1	AAP92030	Aap92030	Sequence
45	738	96.3	266	1	AAP90147	Aap90147	Sequence

OM protein - protein search, using sw model

Run on: April 15, 2005, 15:35:14 ; Search time 22 Seconds
(without alignments)
502.185 Million cell updates/sec

Title: US-09-825-423C-3
Perfect score: 766
Sequence: 1 GSHMSPVFTDNSSPPAVPQS.....TVLDQAETAGARLVVLATAT 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	743	97.0	631	3	US-09-128-314-2	Sequence 2, Appli
2	743	97.0	638	3	US-09-288-391-25	Sequence 25, Appl
3	743	97.0	687	1	US-08-188-281B-14	Sequence 14, Appl
4	743	97.0	687	5	PCT-US94-07280-14	Sequence 14, Appl
5	743	97.0	687	5	PCT-US95-01087-14	Sequence 14, Appl
6	743	97.0	1648	1	US-08-188-281B-12	Sequence 12, Appl
7	743	97.0	1648	5	PCT-US94-07280-12	Sequence 12, Appl
8	743	97.0	1648	5	PCT-US95-01087-12	Sequence 12, Appl
9	743	97.0	3011	1	US-08-188-281B-1	Sequence 1, Appli
10	743	97.0	3011	1	US-08-453-552-1	Sequence 1, Appli
11	743	97.0	3011	2	US-08-710-637-1	Sequence 1, Appli

12	743	97.0	3011	3	US-08-811-566-20	Sequence 20, Appl
13	743	97.0	3011	3	US-09-014-416-1	Sequence 1, Appli
14	743	97.0	3011	3	US-09-014-416-5	Sequence 5, Appli
15	743	97.0	3011	3	US-09-034-756-20	Sequence 20, Appl
16	743	97.0	3011	4	US-09-952-572-9	Sequence 9, Appli
17	743	97.0	3011	5	PCT-US93-00907-1	Sequence 1, Appli
18	743	97.0	3011	5	PCT-US94-07280-1	Sequence 1, Appli
19	743	97.0	3011	5	PCT-US95-01087-1	Sequence 1, Appli
20	743	97.0	3012	3	US-08-811-566-2	Sequence 2, Appli
21	743	97.0	3012	3	US-09-034-756-2	Sequence 2, Appli
22	742	96.9	3011	1	US-08-453-552-2	Sequence 2, Appli
23	742	96.9	3011	2	US-08-710-637-2	Sequence 2, Appli
24	742	96.9	3011	5	PCT-US93-00907-2	Sequence 2, Appli
25	741	96.7	278	4	US-08-635-886C-267	Sequence 267, App
26	741	96.7	278	4	US-08-974-690C-267	Sequence 267, App
27	738	96.3	266	3	US-08-444-818-32	Sequence 32, Appl
28	738	96.3	266	3	US-08-850-328-7	Sequence 7, Appli
29	738	96.3	272	1	US-08-350-884-84	Sequence 84, Appl
30	738	96.3	272	1	US-08-709-173-84	Sequence 84, Appl
31	738	96.3	272	2	US-08-709-177-84	Sequence 84, Appl
32	738	96.3	278	4	US-08-635-886C-265	Sequence 265, App
33	738	96.3	278	4	US-08-974-690C-265	Sequence 265, App
34	738	96.3	344	4	US-10-173-480-20	Sequence 20, Appl
35	738	96.3	349	4	US-10-173-480-25	Sequence 25, Appl
36	738	96.3	350	4	US-10-173-480-18	Sequence 18, Appl
37	738	96.3	355	4	US-10-173-480-40	Sequence 40, Appl
38	738	96.3	358	4	US-10-173-480-36	Sequence 36, Appl
39	738	96.3	364	4	US-10-173-480-32	Sequence 32, Appl
40	738	96.3	367	4	US-10-173-480-38	Sequence 38, Appl
41	738	96.3	424	4	US-10-173-480-28	Sequence 28, Appl
42	738	96.3	465	2	US-08-833-678A-2	Sequence 2, Appli
43	738	96.3	465	3	US-08-529-169A-2	Sequence 2, Appli
44	738	96.3	465	4	US-09-483-799-2	Sequence 2, Appli
45	738	96.3	513	3	US-08-867-611-59	Sequence 59, Appl

OM protein - protein search, using sw model

Run on: April 15, 2005, 15:48:38 ; Search time 137 Seconds
(without alignments)
359.057 Million cell updates/sec

Title: US-09-825-423C-3
Perfect score: 766
Sequence: 1 GSHMSPVFTDNSSPPAVPQS.....TVLDQAETAGARLVVLATAT 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	766	100.0	148	11	US-09-825-423C-3	Sequence 3, Appli
2	766	100.0	241	11	US-09-825-423C-6	Sequence 6, Appli
3	766	100.0	288	11	US-09-825-423C-5	Sequence 5, Appli
4	743	97.0	263	9	US-09-921-397-85	Sequence 85, Appl
5	743	97.0	631	11	US-09-825-423C-1	Sequence 1, Appli
6	743	97.0	3011	9	US-09-742-659-4	Sequence 4, Appli
7	743	97.0	3011	9	US-09-238-076-20	Sequence 20, Appl
8	743	97.0	3011	9	US-09-952-572-9	Sequence 9, Appli
9	743	97.0	3011	9	US-09-747-419-20	Sequence 20, Appl
10	743	97.0	3011	10	US-09-891-894-3	Sequence 3, Appli
11	743	97.0	3011	10	US-09-995-937-20	Sequence 20, Appl
12	743	97.0	3011	10	US-09-917-563-20	Sequence 20, Appl
13	743	97.0	3011	14	US-10-259-275-20	Sequence 20, Appl
14	743	97.0	3011	14	US-10-184-150-3	Sequence 3, Appli
15	743	97.0	3011	15	US-10-328-997-3	Sequence 3, Appli
16	743	97.0	3011	15	US-10-189-359-14	Sequence 14, Appl
17	743	97.0	3012	9	US-09-238-076-2	Sequence 2, Appli
18	743	97.0	3012	10	US-09-995-937-2	Sequence 2, Appli
19	743	97.0	3012	10	US-09-917-563-2	Sequence 2, Appli
20	742	96.9	3011	15	US-10-296-734-406	Sequence 406, App
21	741	96.7	278	15	US-10-651-165-267	Sequence 267, App
22	738	96.3	272	10	US-09-884-456-84	Sequence 84, Appl
23	738	96.3	272	10	US-09-884-455-84	Sequence 84, Appl
24	738	96.3	278	15	US-10-651-165-265	Sequence 265, App
25	738	96.3	344	14	US-10-173-480-20	Sequence 20, Appl
26	738	96.3	344	16	US-10-753-910-20	Sequence 20, Appl
27	738	96.3	349	14	US-10-173-480-25	Sequence 25, Appl
28	738	96.3	349	16	US-10-753-910-25	Sequence 25, Appl
29	738	96.3	350	14	US-10-173-480-18	Sequence 18, Appl
30	738	96.3	350	16	US-10-753-910-18	Sequence 18, Appl
31	738	96.3	355	14	US-10-173-480-40	Sequence 40, Appl
32	738	96.3	355	16	US-10-753-910-40	Sequence 40, Appl
33	738	96.3	358	14	US-10-173-480-36	Sequence 36, Appl
34	738	96.3	358	16	US-10-753-910-36	Sequence 36, Appl
35	738	96.3	364	14	US-10-173-480-32	Sequence 32, Appl
36	738	96.3	364	16	US-10-753-910-32	Sequence 32, Appl
37	738	96.3	367	14	US-10-173-480-38	Sequence 38, Appl
38	738	96.3	367	16	US-10-753-910-38	Sequence 38, Appl
39	738	96.3	424	14	US-10-173-480-28	Sequence 28, Appl
40	738	96.3	424	16	US-10-753-910-28	Sequence 28, Appl
41	738	96.3	465	14	US-10-232-643-2	Sequence 2, Appli
42	738	96.3	473	10	US-09-847-670-1	Sequence 1, Appli
43	738	96.3	473	11	US-09-847-670-1	Sequence 1, Appli
44	738	96.3	631	14	US-10-232-643-1	Sequence 1, Appli
45	738	96.3	686	9	US-09-881-654-2	Sequence 2, Appli

OM protein - protein search, using sw model

Run on: April 15, 2005, 15:41:42 ; Search time 16 Seconds
 (without alignments)
 890.005 Million cell updates/sec

Title: US-09-825-423C-3
 Perfect score: 766
 Sequence: 1 GSHMSPVFTDNSSPPAVPQS.....TVLDQAETAGARLVVLATAT 148

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	741	96.7	3011	1	S40770	genome polyprotein
2	738	96.3	3011	1	GNWVC3	genome polyprotein
3	732	95.6	3010	1	GNWVTC	genome polyprotein
4	728	95.0	3010	1	GNWVTW	genome polyprotein
5	727	94.9	3010	1	A45573	genome polyprotein
6	727	94.9	3011	1	GNWVCH	genome polyprotein
7	723	94.4	3010	1	S18030	genome polyprotein
8	716	93.5	3010	1	GNWVCJ	genome polyprotein
9	682	89.0	3014	1	JC5620	genome polyprotein
10	674	88.0	3033	1	JQ1303	genome polyprotein
11	669	87.3	3033	1	GNWVJ8	genome polyprotein
12	601.5	78.5	386	2	S68016	ATPase/RNA helicase
13	327	42.7	3005	2	T08841	polyprotein - dour

14	322	42.0	216	2	S21337	genome polyprotein
15	319	41.6	876	2	PC2219	polypeptide - hepa
16	300.5	39.2	2970	2	T08839	polyprotein - marm
17	116.5	15.2	3054	1	GNBVEV	genome polyprotein
18	115.5	15.1	823	2	B70203	ATP-dependent heli
19	112.5	14.7	1087	2	D84767	probable pre-mRNA
20	106.5	13.9	735	2	S37903	probable ATP-depen
21	106.5	13.9	968	2	T46568	ATP-dependent RNA
22	105	13.7	3125	1	GNVSPP	genome polyprotein
23	105	13.7	3140	1	GNVSRA	genome polyprotein
24	105	13.7	3140	2	S47508	genome polyprotein
25	105	13.7	3141	1	GNVSPD	genome polyprotein
26	103	13.4	3066	1	JQ1662	genome polyprotein
27	99	12.9	1090	2	C86450	F5D14.27 protein -
28	99	12.9	3066	1	JQ1661	genome polyprotein
29	98.5	12.9	3068	1	A44062	genome polyprotein
30	98	12.8	634	2	T01408	inclusion protein
31	97.5	12.7	634	2	A48335	cytoplasmic inclus
32	97.5	12.7	3061	1	JN0545	genome polyprotein
33	97.5	12.7	3063	2	JS0166	genome polyprotein
34	97.5	12.7	3163	1	JQ1895	genome polyprotein
35	97	12.7	1152	2	H88533	probable ATP-depen
36	97	12.7	3206	1	GNVSPV	genome polyprotein
37	96	12.5	833	2	E82708	ATP-dependent heli
38	95.5	12.5	813	2	E87396	helicase, probable
39	95	12.4	3898	1	A44217	genome polyprotein
40	95	12.4	3988	1	GNWVBV	genome polyprotein
41	94	12.3	3432	1	GNWVJS	genome polyprotein
42	94	12.3	3432	1	GNWVJE	genome polyprotein
43	93.5	12.2	3005	1	GNVSTV	genome polyprotein
44	93	12.1	838	2	B83150	probable ATP-depen
45	93	12.1	3341	1	A42996	genome polyprotein

OM protein - protein search, using sw model

Run on: April 15, 2005, 15:42:38 ; Search time 189 Seconds
 (without alignments)
 400.993 Million cell updates/sec

Title: US-09-825-423C-3
 Perfect score: 766
 Sequence: 1 GSHMSPVFTDNSSPPAVPQS.....TVLDQAETAGARLVVLATAT 148

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	743	97.0	658	2	Q68K34	Q68k34 hepatitis c
2	743	97.0	659	2	Q68K31	Q68k31 hepatitis c
3	743	97.0	659	2	Q68K32	Q68k32 hepatitis c
4	743	97.0	659	2	Q68K40	Q68k40 hepatitis c
5	743	97.0	659	2	Q68K42	Q68k42 hepatitis c
6	743	97.0	659	2	Q68K55	Q68k55 hepatitis c
7	743	97.0	659	2	Q68K59	Q68k59 hepatitis c
8	743	97.0	659	2	Q68K62	Q68k62 hepatitis c
9	743	97.0	2908	2	Q6IX04	Q6ix04 hepatitis c
10	743	97.0	3011	2	O36579	O36579 hepatitis c
11	743	97.0	3011	2	O36608	O36608 hepatitis c
12	743	97.0	3011	2	O36610	O36610 hepatitis c
13	743	97.0	3011	2	Q9ELS8	Q9els8 hepatitis c
14	743	97.0	3015	2	Q9PWU9	Q9pwu9 hepatitis c
15	743	97.0	3015	2	Q9PWX5	Q9pwx5 hepatitis c

16	742	96.9	652	2	Q68K51	Q68k51 hepatitis c
17	742	96.9	658	2	Q68K66	Q68k66 hepatitis c
18	742	96.9	659	2	Q68K30	Q68k30 hepatitis c
19	742	96.9	659	2	Q68K33	Q68k33 hepatitis c
20	742	96.9	659	2	Q68K49	Q68k49 hepatitis c
21	742	96.9	659	2	Q68K56	Q68k56 hepatitis c
22	741	96.7	660	2	Q68K38	Q68k38 hepatitis c
23	741	96.7	660	2	Q68K63	Q68k63 hepatitis c
24	741	96.7	3011	2	Q03463	Q03463 hepatitis c
25	739	96.5	658	2	Q68K61	Q68k61 hepatitis c
26	739	96.5	659	2	Q68K39	Q68k39 hepatitis c
27	739	96.5	659	2	Q68K41	Q68k41 hepatitis c
28	739	96.5	659	2	Q68K47	Q68k47 hepatitis c
29	739	96.5	3011	2	Q9DIT6	Q9dit6 hepatitis c
30	738	96.3	659	2	Q68K37	Q68k37 hepatitis c
31	738	96.3	659	2	Q68K68	Q68k68 hepatitis c
32	738	96.3	2436	2	Q81756	Q81756 hepatitis c
33	738	96.3	3011	1	POLG_HCV1	P26664 h genome po
34	738	96.3	3011	2	O36609	O36609 hepatitis c
35	738	96.3	3011	2	Q9IFE5	Q9ife5 hepatitis c
36	737	96.2	659	2	Q68K67	Q68k67 hepatitis c
37	736	96.1	636	2	Q68K64	Q68k64 hepatitis c
38	736	96.1	659	2	Q68K35	Q68k35 hepatitis c
39	736	96.1	659	2	Q68K43	Q68k43 hepatitis c
40	735	96.0	3010	2	Q9QIX1	Q9qix1 hepatitis c
41	735	96.0	3010	2	Q9QIX2	Q9qix2 hepatitis c
42	734	95.8	629	2	Q9WJT2	Q9wjt2 hepatitis c
43	734	95.8	630	2	O93090	O93090 hepatitis c
44	734	95.8	652	2	Q68K53	Q68k53 hepatitis c
45	734	95.8	1984	2	Q7T4V8	Q7t4v8 hepatitis c